

Reviewer Report

Title: High-quality *Schistosoma haematobium* genome achieved by single-molecule and long-range sequencing

Version: Original Submission **Date:** 6/5/2019

Reviewer name: Krystyna Cwiklinski

Reviewer Comments to Author:

The manuscript by Stroehlein and colleagues reports the improved genome assembly for the blood fluke *Schistosoma haematobium*. This study complements the sequence data currently available for *Schistosoma* parasites. In particular, this study is enhanced by the methodology used by the authors to use the single molecule and long-range sequence data to improve upon the current *S. haematobium* assembly and to consolidate the gene model information. This allows research continuity providing an important future resource.

The manuscript is well written and is suitable for publication in GigaScience as a data note following minor clarification/revision.

1. Although discussed throughout the main body of the manuscript, further emphasis is required in the abstract to reflect that the sequencing carried out as part of this study was not used to assemble a wholly new version of the genome but instead was used to improve the version 1 assembly. The gene model mapping should also be included.
2. Line 182 - can the authors provide further clarification regarding the unscaffolded contigs used in the Dovetail HiRise pipeline - were these the contigs used for the version 1 scaffold assembly or the contigs that did not scaffold in the original version?
3. Lines 288-292 - where are the genomes publicly available? If WormBase ParaSite, mention which version of the genomes were used for the phylogenetic analysis.

Level of Interest

Please indicate how interesting you found the manuscript: Choose an item.

Quality of Written English

Please indicate the quality of language in the manuscript: Choose an item.

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